‘hagis’, an R Package Resource for Pathotype Analysis of *Phytophthora sojae* Populations Causing Stem and Root Rot of Soybean

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14 August, 2019

*Phytophthora sojae* is a significant pathogen of soybean worldwide. Pathotype surveys for *Phytophthora sojae* are conducted to monitor resistance gene efficacy and determine if new resistance genes are needed. Valuable measurements for pathotype analysis include the distribution of susceptible reactions, pathotype complexity, pathotype frequency, and diversity indices for pathotype distributions. Previously the Habgood-Gilmour Spreadsheet (HaGiS), written in Microsoft® Excel, was used for data analysis. However, the growing popularity of the R programming language in plant pathology and desire for reproducible research made HaGiS a prime candidate for conversion into an R package. Here we report on the development and use of an R package, ‘hagis’, that can be used to produce all outputs from the HaGiS Excel sheet for *P. sojae* or other gene-for-gene pathosystem studies.

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# R Package Announcement

Uniform and healthy stand establishment is essential to maximizing soybean (*Glycine max*) yield. Oomycetes such as *Phytophthora sojae* constitute a significant threat to stand establishment and yield. *Phytophthora sojae* has been managed primarily via deployment of single resistance genes in commercial soybean cultivars, which interact with *P. sojae* *Avr* gene products to confer resistance (Anderson et al. 2015). Genetic resistance to *P. sojae* is the most economical form of control for *P. sojae* as it confers season-long protection to non-compatible pathotypes (Dorrance et al. 2016). However, *P. sojae* pathotype surveys need to be regularly conducted to determine shifts in pathotypes over time and provide recommendations for effective resistance genes. Although state-wide pathotype surveys have been conducted for the past 60 years in the USA, there has been no significant advance in pathotype analysis since the development of the Habgood-Gilmour Spreadsheet (HaGiS), written in Microsoft® Excel, in 1999 (Herrmann et al. 1999; Kaufmann and Gerdemann 1958).

*Phytophthora sojae* pathotype surveys monitor the efficacy of soybean resistance genes in relation to *P. sojae* population(s). In doing so, large sets of virulence data are generated, potentially for hundreds of isolates (Dorrance et al. 2016). Using such large datasets within the HaGiS Excel-based program can be cumbersome and time intensive to transfer the data into and perform analysis. The R statistical programming language (R Core Team 2019) offers the ability to work with large data sets in an easy and efficient manner without additional data entry steps that the HaGiS Excel program requires, while treating the virulence data as read-only, thereby further reducing the chance for errors.

R has become widely used in plant pathology studies due to its open-source framework and amenability to conduct reproducible research (Sparks et al. 2011; Duku et al. 2016; Bergna et al. 2018; Wallace et al. 2018). Using an R package for analyzing pathotype survey data can replicate all analyses provided by Excel-based programs. It allows users to create reproducible research and more detailed visualizations as well as allowing the plant pathology community to actively contribute to and build upon this code for future studies. For instance, McCoy and Noel (2018) produced R scripts to conduct these analyses originally performed with HaGiS, which were used to create the ‘hagis’ R package (McCoy et al. 2019).

For ease of use the package uses a single argument format, which works in all ‘hagis’ functions. Users provide their own data in the form of a spreadsheet, CSV or text file, specifying the proper fields for analysis. Functions are provided to calculate pathotype complexity and summarize the distribution of reactions for each gene tested. Simple, Shannon, Simpson, Gleason and Evenness diversity indices are calculated for the pathotype data set. Outputs from these analyses are given in publication ready graphics or tables and can be further modified by the user, *e.g.*, Table 1.

The R language offers many advantages to Excel-based data analysis such as reproducibility and user customization. Furthermore, ‘hagis’ takes advantage of the ‘data.table’ package (Dowle and Srinivasan 2019) to efficiently handle large data sets such as those produced through *P. sojae* pathotype surveys rapidly and efficiently. Significantly, ‘hagis’ provides the first development in *P. sojae* pathotype analysis in 20 years. While ‘hagis’ was developed to support *P. sojae* pathotype surveys, it was designed to work with any pathotype analyses of gene-for-gene pathosystems to determine effective resistance genes in management.

The package source code, including the Rmarkdown code for this paper, more information and instructions on how to use ‘hagis’ can be found at <https://openplantpathology.github.io/hagis/>. The package can be downloaded and installed from the Comprehensive R Archive Network (CRAN) website (<https://CRAN.R-project.org/package=hagis>) and is released under the MIT licence.

**Table 1.** Example of tabular output from ‘hagis’’s summarize\_gene() at 60 % susceptibility cut-off. This function produces a detailed table displaying the number of isolates each gene is susceptible to, as well as offering a percentage of the isolates tested which are pathogenic on each gene.

|  |  |  |
| --- | --- | --- |
| **Gene** | **No. Susceptible** | **Perc. Pathogenic** |
| susceptible | 21 | 100 |
| 1a | 21 | 100 |
| 1b | 15 | 71.43 |
| 1c | 20 | 95.24 |
| 1d | 16 | 76.19 |
| 1k | 18 | 85.71 |
| 2 | 14 | 66.67 |
| 3a | 5 | 23.81 |
| 3b | 20 | 95.24 |
| 3c | 4 | 19.05 |
| 4 | 5 | 23.81 |
| 5 | 13 | 61.9 |
| 6 | 11 | 52.38 |
| 7 | 21 | 100 |

# Acknowledgements

Funding for this work was provided by: Michigan Soybean Promotion Committee, Project GREEEN, North Central Soybean Research Program, and GRDC Project DAQ00186 - Improving Grower Surveillance, Management Epidemiology Knowledge And Tools To Manage Crop Disease

# Literature Cited

Anderson, R. G., Deb, D., Fedkenheuer, K., and McDowell, J. M. 2015. Recent progress in RXLR effector research. Molecular Plant-Microbe Interactions. 28:1063–1072

Bergna, A., Cernava, T., Rändler, M., Grosch, R., Zachow, C., and Berg, G. 2018. Tomato seeds preferably transmit plant beneficial endophytes. Phytobiomes Journal. 2:183–193

Dorrance, A. E., Kurle, J., Robertson, A. E., Bradley, C. A., Giesler, L., Wise, K., and Concibido, V. C. 2016. Pathotype diversity of *phytophthora sojae* in eleven states in the United States. Plant Disease. 100:1429–1437

Dowle, M., and Srinivasan, A. 2019. *data.table: Extension of ‘data.frame‘*.

Duku, C., Sparks, A. H., and Zwart, S. J. 2016. Spatial modelling of rice yield losses in Tanzania due to bacterial leaf blight and leaf blast in a changing climate. Climatic Change. 135:569–583

Herrmann, A., Lower, C. F., and Schachtel, G. A. 1999. A new tool for entry and analysis of virulence data for plant pathogens [correspondence]. Plant Pathology.

Kaufmann, M. J., and Gerdemann, J. W. 1958. Root and stem rot of soybean caused by *Phytophthora sojae* n. Sp. Phytopathology. 48

McCoy, A., and Noel, Z. 2018. AGmccoy/Phytopthora-sojae-Pathotype-analysis: Beta-release of *Phytophthora sojae* pathotype analysis code.

McCoy, A., Noel, Z., Sparks, A. H., and Chilvers, M. 2019. *hagis: Analysis of plant pathogen pathotype complexities, distributions and diversity*.

R Core Team. 2019. *R: A language and environment for statistical computing*. R Foundation for Statistical Computing, Vienna, Austria.

Sparks, A. H., Forbes, G. A., Hijmans, R. J., and Garrett, K. A. 2011. A metamodeling framework for extending the application domain of process-based ecological models. Ecosphere. 2:art90

Wallace, J. G., Kremling, K. A., Kovar, L. L., and Buckler, E. S. 2018. Quantitative genetics of the maize leaf microbiome. Phytobiomes Journal. 2:208–224